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CLAIM AMENDMENTS

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Please amend the claims as follows:

- 1. (Currently amended) A substantially purified nucleic acid molecule selected from the group consisting of:
 - (a) nucleic acid molecules encoding a phytol-kinase polypeptide or polypeptide having phytol-kinase activity;
 - (b) nucleic-acid molecules encoding a plant-phytol kinase polypeptide, or a plant polypeptide having phytol kinase activity;
 - (c) nucloie-acid molecules encoding a syanobacterial phytol-kinase polypeptide or a syanobacterial polypeptide having phytol-kinase activity;
 - (d) (a) a nucleic acid molecules molecule encoding a phytol kinase polypeptide, or a pelypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 2, 6, 20-68, and 79;
 - (e) nucleic acid molecules encoding a plant phytol kinase polypeptide, or a plant polypeptide having phytol kinase activity, comprising an amino acid selected from the group consisting of SEQ ID NOs: 2, 6, and 37-68;
 - (f) nucleic acid molecules encoding a cyanobacterial phytol kinase polypeptide, or a cyanobacterial polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-27, 29-34, and 79;
 - (g) nucleic-acid molecules encoding a plant phytol kinase polypeptide, or a plant polypeptide having phytol kinase activity, comprising an amino acid selected from the group consisting of SEQ ID NOs: 74, 77, and 78;
 - (h)—nucleic acid molecules encoding a plant phytol kinase polypeptide, or a plant polypeptide having phytol kinase activity, comprising an amino acid solected from the group consisting of SEQ ID NOs: 74, 77, and 78, wherein said polypeptide is not derived from Allium porrum, Brassica napus, Gossypium, Glycine max, Oryza sativa, Sorghum bicolor, Triticum aestivum, and Zea mays;

- (i) nucleic acid molecules encoding a plant phytol kinase-polypeptide, or a plant polypeptide having phytol kinase activity, comprising an amine-acid sequence selected from the group consisting of SEQ-ID-NOs: 74, 77, and 78 and further comprising an amine acid sequence comprising one or more of SEQ-ID-NOs: 75 and 76;
- (j) ... nucleic acid molecules encoding a plant phytol kinase polypeptide, or a plant polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 74, 77, and 78 and further comprising an amino acid sequence comprising one or more of SEQ ID NOs: 75 and 76, wherein said polypeptide is not derived from Allium porrum, Brassica napus, Gossypium, Glycine max, Oryza sativa, Sorghum bicolor, Triticum aestivum, and Zea mays;
- (k) nucleic acid molecules encoding a cyanobacterial phytol kinase polypeptide, or a cyanobacterial polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 71, 72, and 73;
- (1) nucleic acid molecules encoding a cyanobacterial phytol-kinase polypoptide, or a cyanobacterial polypoptide having phytol-kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 71, 72, and 73, wherein said polypoptide is not derived from Syncehocystis, Aquifex acolicus, Chlorobium tepidum, Chloroflexus aurantiacus, Nostoc punctiforme, Prochlorococcus marinus, Rickettsia conorii, Rickettsia prowazekii, Rickettsia sibirica, Syncehoccus, Thermosynechoccus elongatus, Trichodesmium erythracum and Saccharomyces cerevisiae;
- (m) nucleic acid-molecules encoding a cyanobacterial phytol kinase polypeptide, or a cyanobacterial polypeptide having phytol kinase activity, comprising one or more amino acid sequences selected from the group consisting of SEQ-ID NOs: 71, 72, and 73-and further comprising an amino acid sequence comprising one or more of SEQ-ID NOs: 69 and 70;
- (n) nucleie-acid-molecules encoding a cyanobacterial phytol-kinase-polypeptide, or a cyanobacterial-polypeptide having phytol-kinase-activity, comprising one or more amino acid sequences selected from the group consisting of SEQ-ID NOs: 71, 72, and 73 and further-comprising an amino acid sequence comprising one or more of SEQ-ID-NOs: 69

and 70, wherein said polypeptide is not derived from Synechocystis, Aquifex acolicus, Chlorobium tepidum, Chloroflexus aurantiacus, Nostoc punetiforme, Prochlorococcus marinus, Rickettsia-conorii, Rickettsia prowazekii, Rickettsia sibirica, Synechocous, Thermosynechoccus—elongatus,—Trichodesmium—erythraeum—and Saccharomyees cerevisiae:

- (o) nucleic acid molecules encoding a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-41-and 53-68;
- (p) nucleic acid molecules encoding a yeast phytol kinase polypeptide, or a yeast polypeptide having phytol kinase activity; and
- -nuelcic acid molecules encoding a yeast phytol kinase polypeptide, or a yeast polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 35 and 36.
- a nucleic acid molecule encoding a polypeptide having phytol kinase activity and comprising an amino acid sequence with at least about 99% identity to the amino acid sequence of SEO ID NO:2;
- a nucleic acid molecule encoding a polypeptide having phytol kinase activity and comprising a sequence with at least 99% identity to the nucleic acid sequence of SEO ID NO:1; and
- a nucleic acid molecule comprising the nucleic acid sequence of SEQ ID NO:1. (d)

2-3. (Canceled)

- 4. (Currently amended) A DNA construct comprising a heterologous promoter that functions in plants operably linked to the nucleic acid molecule of claim Iselected from the group consisting of:
 - (a) --- nucleic acid molecules one oding a polypoptide comprising an amino acid sequence having at least about 70% identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 6, 20-68, and 79;

- (b) nucleic acid molecules encoding a polypeptide comprising an amino acid sequence having at least about 80% identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 6, 20 68, and 79;
- (c) nucleic acid molecules encoding a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 6, 20-68, and 79;
- (d) nucleic acid molecules encoding a polypeptide comprising—an amino acid sequence having at least about 95% identity to an amino acid sequence selected from the group consisting of SEQ ID NO: 2, 6, 20 68; and 79;
- (e) nucleic acid molecules encoding—a polypeptide comprising an amino acid sequence having at least about 99% identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 6, 20-68, and 79;
- (f) nucleic acid molecules comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1, 5, and 17;
- (g) nucleic acid molecules comprising a nucleic acid sequence having at least about 80% identity to a nucleic acid sequence selected from the group-consisting of SEQ ID NOs: 1, 5, and 17;
- (h) nucleic acid molecules comprising a nucleic acid sequence having at least about 90% identity to a nucleic acid sequence selected from the group consisting of SEQ-ID NOs: 1, 5, and 17;
- (i) nucleic acid molecules comprising a nucleic acid sequence having at least about 95%-identity to a nucleic acid sequence selected from the group consisting of SEQ-ID NOs: 1, 5, and 17;
- (j) nucleic acid molecules comprising a nucleic acid sequence having at least about 99% identity to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1, 5, and 17;
- (k) nucleic acid molecules encoding a phytol kinase polypeptide or polypeptides having phytol kinase activity;

- (l) nucleic acid molecules encoding a plant-phytol kinase polypeptide, or a plant polypeptide having phytol kinase activity;
- (m) —nucleic acid molecules encoding a cyanobacterial phytol kinase polypeptide or a cyanobacterial polypeptide having phytol kinase activity;
- (n) nucleic acid-molecules encoding a phytol kinase polypeptide, or a polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 6, 20-68, and 79;
- (o) nucleic acid-molecules encoding a plant phytol kinase polypeptide, or a plant polypeptide having phytol-kinase activity, comprising an amino acid selected-from the group consisting of SEQ ID NOs: 2, 6, and 37 68;
- (p) nucleic acid molecules encoding a cyanobacterial phytol kinase polypeptide, or a cyanobacterial polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-27, 29-34, and 79;
- (q) nucleic acid molecules encoding a plant-phytol kinase polypeptide, or a plant polypeptide having phytol kinase activity, comprising an amine acid selected from the group consisting of SEQ ID NOs: 74, 77, and 78;
- (r) nucleic acid molecules encoding a plant phytol kinase polypeptide, or a plant polypeptide having phytol kinase activity, comprising an amino acid-selected from the group consisting of SEQ ID NOs: 74, 77, and 78, wherein said polypeptide is not derived from Allium porrum, Brassica napus, Gossypium, Glycine-max, Oryza sativa, Sorghum bicolor, Triticum aestivum, and Zea mays;
- (s) nucleic acid molecules encoding a plant phytol-kinase polypeptide, or a plant polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 74, 77, and 78 and further comprising an amino acid sequence comprising one or more of SEQ ID NOs: 75 and 76;
- (t) nucleic acid melecules encoding a plant-phytol kinase polypeptide, or a plant polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 74, 77, and 78 and further comprising an amino acid sequence comprising one or more of SEQ ID NOs: 75 and 76, wherein said

polypeptide is not derived from Allium porruin, Brassica napus, Gossypium, Glycine max, Oryza sativa, Sorghum bicolor, Triticum aestivum, and Zea mays;

- (u) nucleic acid molecules encoding a cyanobacterial phytol kinase polypeptide, or a cyanobacterial polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 71, 72, and 73;
- (v) nucleic acid molecules encoding a oyanobacterial-phytol kinase polypeptide, or a eyanobacterial polypeptide having-phytol kinase activity, comprising an amino-acid sequence selected from the group consisting of SEQ ID NOs: 71, 72, and 73, wherein said polypeptide is not derived from Synechocystis, Aquifex acolicus, Chlorobium tepidum, Chloroflexus aurantiacus, Nostoc punctiforme, Prochlorococcus marinus, Rickettsia conorii, Rickettsia prowazekii, Rickettsia sibirica, Synechoccus, Thermosynechoccus elongatus, Trichodesmium erythracum and Saccharomyces cerevisiae;
- (w) nucleic acid molecules encoding a cyanobacterial phytol kinase polypeptide, or a cyanobacterial polypeptide having phytol kinase activity, comprising one or more amino acid sequences selected from the group consisting of SEQ ID NOs: 71, 72, and 73 and further comprising an amino acid sequence comprising one or more of SEQ ID NOs: 69 and 70;
- (x)—nucleic acid molecules encoding a cyanobacterial phytol kinase polypeptide; or a eyanobacterial polypeptide having phytol kinase activity, comprising one or more amino acid sequences selected from the group consisting of SEQ-ID NOs: 71, 72, and 73 and further comprising an amine acid sequence comprising one or more of SEQ-ID NOs: 69 and 70, wherein said polypeptide is not derived from Synechocystis, Aquifex-acolicus, Chlorobium-tepidum, Chloroflexus aurantiacus, Nostoc punctiforme, Prochlorococcus marinus, Rickettsia conorii, Rickettsia prowazekii, Rickettsia sibirica, Synechoccus, Thermosynechoccus—clongatus, Trichodesmium—crythraeum—and—Saccharomyces ecrevisiae;
- (y) nucleic-acid molecules encoding a yeast-phytol kinase-polypeptide, or a yeast polypeptide having phytol kinase activity;

- (2) nucleic acid molecules encoding a yeast phytol kinase polypeptide, or a yeast polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 35 and 36; and
- (aa) nucleic acid molecules encoding a polypoptide comprising an amine acid sequence selected from the group consisting of SEQ ID NOs: 20 41 and 53-68.
- 5. (Previously Presented) A transformed plant comprising the nucleic acid molecule of claim 1.
- 6. (Original) The transformed plant of claim 5, wherein said plant is selected from the group consisting of alfalfa, Arabidopsis thaliana, barley, Brassica campestris, oilseed rape, broccoli, cabbage, citrus, canola, cotton, garlic, oat, Allium, flax, an ornamental plant, peanut, pepper, potato, rapeseed, rice, rye, sorghum, strawberry, sugarcane, sugarbeet, tomato, wheat, poplar, pine, fir, eucalyptus, apple, lettuce, lentils, grape, banana, tea, turf grasses, sunflower, soybean, chick peas, corn, Phaseolus, crambe, mustard, castor bean, sesame, cottonseed, linseed, safflower, and oil palm.
- 7. (Original) The transformed plant of claim 5, wherein said plant is selected from the group consisting of canola, oilseed rape, and soybean.
- 8. (Withdrawn) The transformed plant of claim 5, wherein said transformed plant comprises tissue with at least one of altered tocopherol and tocotrienol levels relative to a plant with a similar genetic background but lacking said nucleic acid molecule.
- 9. (Withdrawn) The transformed plant of claim 5, wherein said transformed plant produces a seed with at least one of increased tocopherol and tocotrienol levels relative to a plant with a similar genetic background but lacking said nucleic acid molecule.
- 10. (Previously Presented) A transformed plant comprising the DNA construct of claim 4.
- 11. (Original) The transformed plant of claim 10, wherein said plant is selected from the group consisting of alfalfa, *Arabidopsis* thaliana, barley, *Brassica campestris*, oilseed rape, broccoli, cabbage, citrus, canola, cotton, garlic, oat, *Allium*, flax, an ornamental plant, peanut, pepper, potato, rapeseed, rice, rye, sorghum, strawberry, sugarcane, sugarbeet, tomato, wheat, poplar, pine, fir, eucalyptus, apple, lettuce, lentils, grape, banana, tea, turf grasses, sunflower,

soybean, chick peas, corn, *Phaseolus*, crambe, mustard, castor bean, sesame, cottonseed, linseed, safflower, and oil palm.

- 12. (Original) The transformed plant of claim 10, wherein said plant is selected from the group consisting of oilseed rape, soybean and canola.
- 13. (Withdrawn) The transformed plant of claim 10, wherein said transformed plant comprises tissue with at least one of altered tocopherol or tocotrienol levels relative to a plant with a similar genetic background but lacking said introduced first nucleic acid molecule.
- 14. (Withdrawn) The transformed plant of claim 10, wherein said transformed plant produces a seed with at least one of increased tocopherol or tocotrienol levels relative to a plant with a similar genetic background but lacking said introduced first nucleic acid molecule.
- 15. (Withdrawn) The transformed plant of claim 10, wherein said transformed plant comprises tissue with at least one of altered tocopherol or tocotrienol levels relative to a plant with a similar genetic background but lacking said introduced first and second nucleic acid molecules.
- 16. (Withdrawn) The transformed plant of claim 10, wherein said transformed plant produces a seed with at least one of increased tocopherol or tocotrienol levels relative to a plant with similar genetic background but lacking said introduced first and second nucleic acid molecules.
- 17. (Previously Presented) The transformed plant of claim 37, wherein the second introduced nucleic acid molecule comprises one or more of SEQ ID NOs: 13-16, and 18 or 19.
- 18. (Withdrawn) A method for increasing at least one of tocopherol and tocotrienol levels in a plant comprising transforming the plant with the DNA construct of claim 4.
- 19. (Withdrawn) The method of claim 18, wherein said plant is selected from the group consisting of alfalfa, Arabidopsis thaliana, barley, Brassica campestris, oilsced rape, broccoli, cabbage, citrus, canola, cotton, garlic, oat, Allium, flax, an ornamental plant, peanut, pepper, potato, rapeseed, rice, rye, sorghum, strawberry, sugarcane, sugarbeet, tomato, wheat, poplar, pine, fir, eucalyptus, apple, lettuce, lentils, grape, banana, tea, turf grasses, sunflower, soybean, chick peas, com, Phaseolus, crambe, mustard, castor bean, sesame, cottonseed, linseed, safflower, and oil palm.

- 20. (Withdrawn) The method of claim 18, wherein said plant is selected from the group consisting of oilseed rape, soybean and canola.
- 21. (Withdrawn) The method of claim 18, wherein said transformed plant comprises tissue with at least one of altered tocopherol or tocotrienol levels relative to a plant with a similar genetic background but lacking said introduced first nucleic acid molecule.
- 22. (Withdrawn) The method of claim 18, wherein said transformed plant produces a seed with at least one of increased tocopherol or tocotrienol levels relative to a plant with a similar genetic background but lacking said introduced first nucleic acid molecule.
- 23. (Withdrawn) The method of claim 3, wherein the second introduced nucleic acid molecule comprises one or more of SEQ ID NOs: 13-16, and 18 or 19.
- 24. (Previously presented) Seed from the plant of claim 10 comprising the DNA construct.

25-29. (Canceled)

- 30. (Withdrawn) A method for increasing the ability of a plant to withstand a stress, the method comprising incorporating into one or more cells of the plant a DNA construct comprising
 - (a) an heterologous promoter;
 - (b) a DNA encoding a phytol kinase; and
 - (c) a 3' untranslated region containing a functional polyadenylation signal wherein expression of the DNA construct increases the ability of the plant to withstand the stress.
- 31. (Withdrawn) A plant cell transformed with a DNA construct encoding a phytol kinase that confers stress to a plant regenerated from said plant cell.
- 32. (Withdrawn) A transgenic plant regenerated from the plant cell of claim 31.
- 33. (Withdrawn) A seed produced by the transgenic plant of claim 32.
- 34. (Withdrawn) The method of claim 26, wherein a DNA molecule encoding a plastid transit peptide is positionally located and operably linked between the promoter and the DNA molecule encoding the phytol kinase.
- 35. (Withdrawn) A method of increasing the production of tocotrienols in a plant comprising:
 (a) transforming a plant cell with a nucleic acid construct which causes the down regulation of

SEQ ID NOs: 1, 5, or 17 or a nucleic acid sequence having at least about 80% identity to such sequence; (b) growing the transformed plant cell into a fertile plant; and (c) selecting for a plant with increased tocotrienol levels.

- 36. (Withdrawn) The method of claim 35 wherein down regulation is accomplished through dsRNAi, antisense suppression or sense suppression.
- 37. (Previously presented) The transformed plant of claim 10, further comprising an introduced second nucleic acid molecule encoding an enzyme selected from the group consisting of MT1, tMT2, GMT, tyrA, HPT, tocopherol cyclase, chlorophyllase, dxs, dxr, GGPPS, HPPD, AANT1, IDI, and GGH.
- 38. (Previously presented) The method of claim 18, further comprising transforming the plant with an introduced second nucleic acid molecule encoding an enzyme selected from the group consisting of MT1, tMT2, GMT, tyrA, HPT, tocopherol cyclase, chlorophyllase, dxs, dxr, GGPPS, HPPD, AANT1, IDI, and GGH.

Please add new claims 39-40

- 39. (New) The nucleic acid molecule of claim 1, wherein the nucleic acid molecule encodes a polypeptide comprising the amino acid sequence of SEQ ID NO: 2.
- 40. (New) The nucleic acid molecule of claim 1, wherein the nucleic acid molecule comprises SEQ ID NO: 1.